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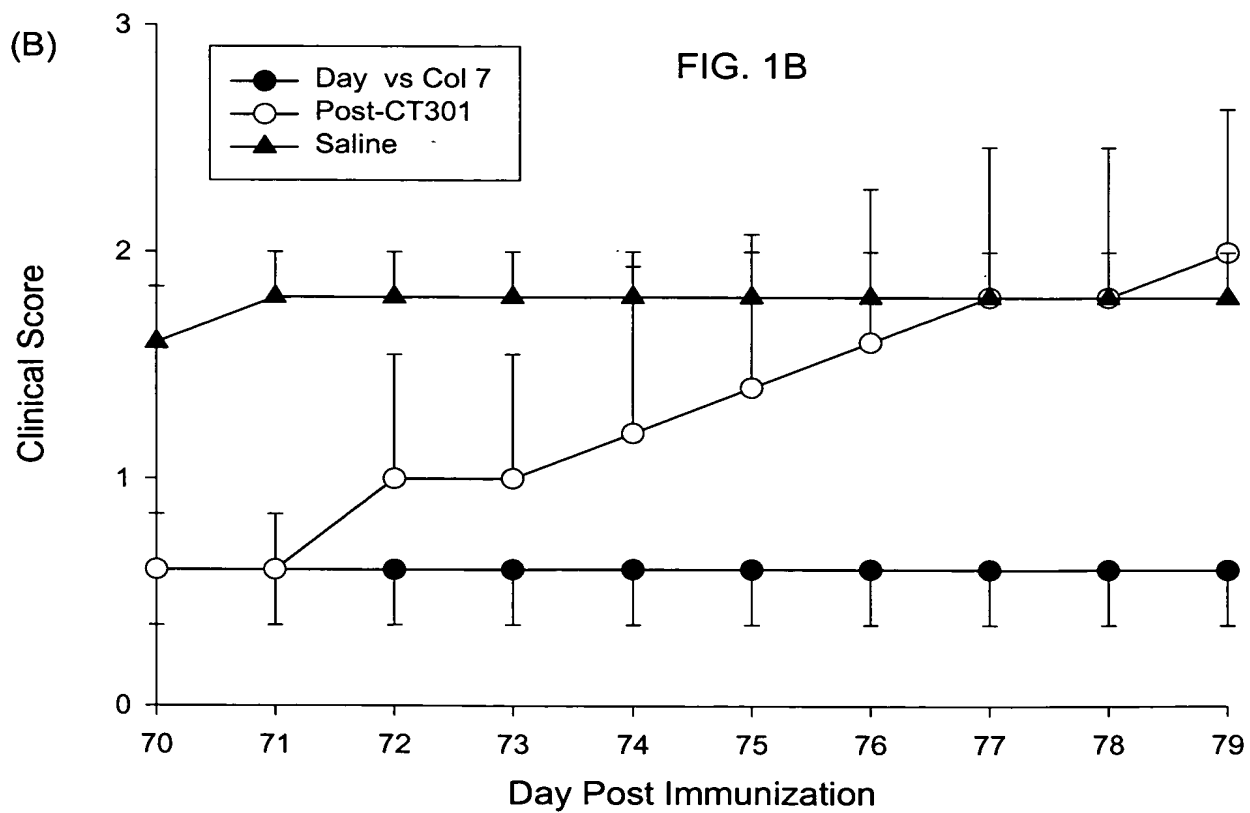
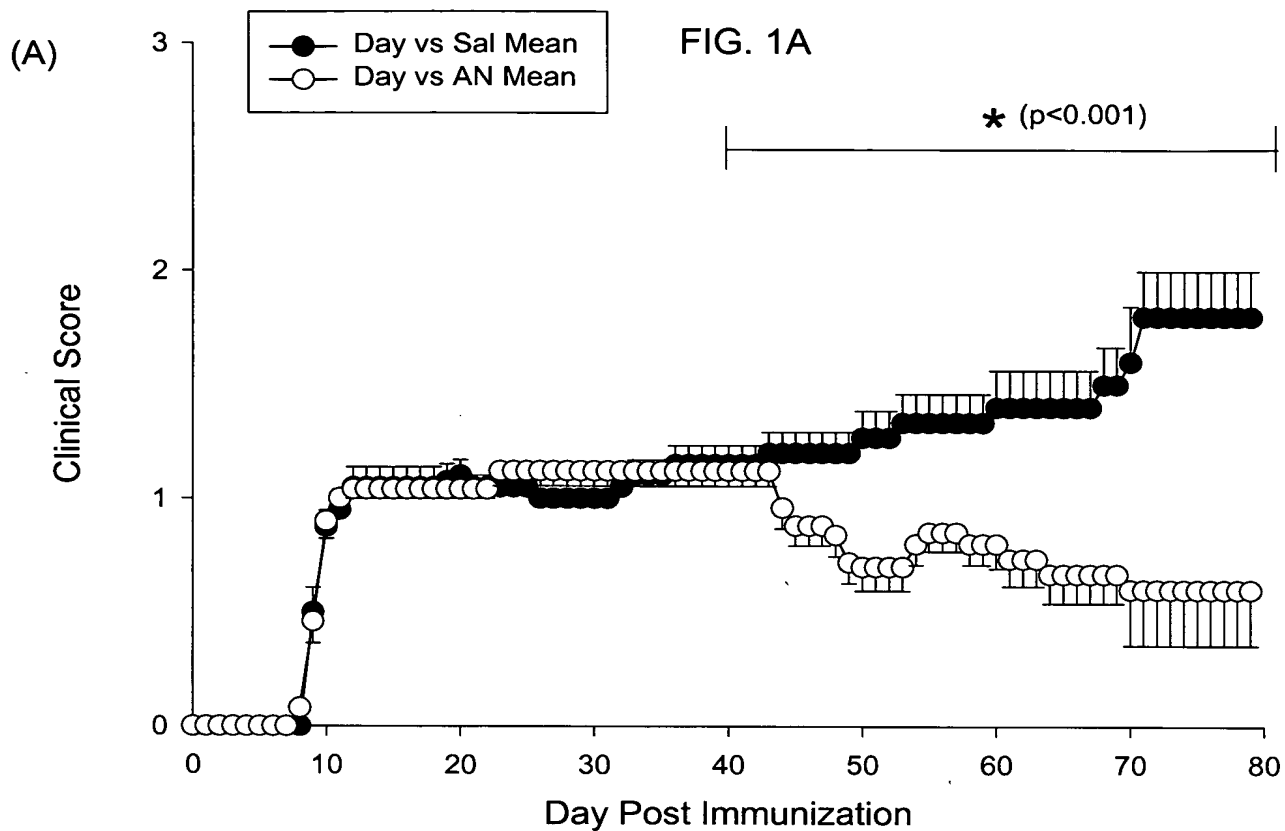




FIG. 2A

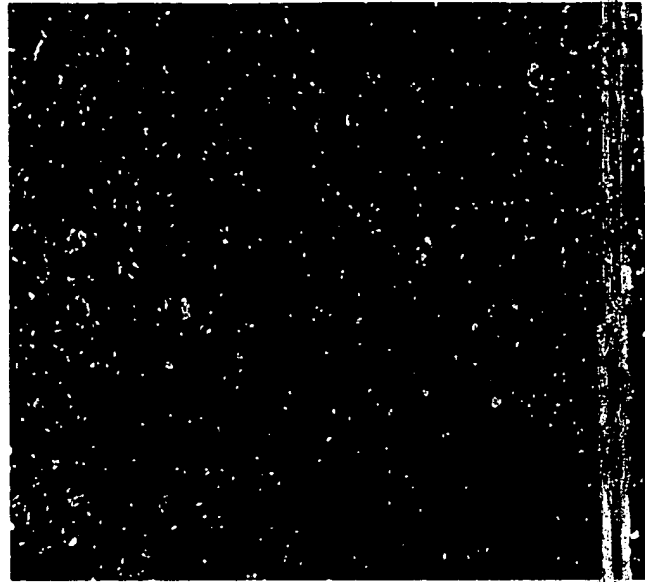


FIG. 2B



FIG. 2C

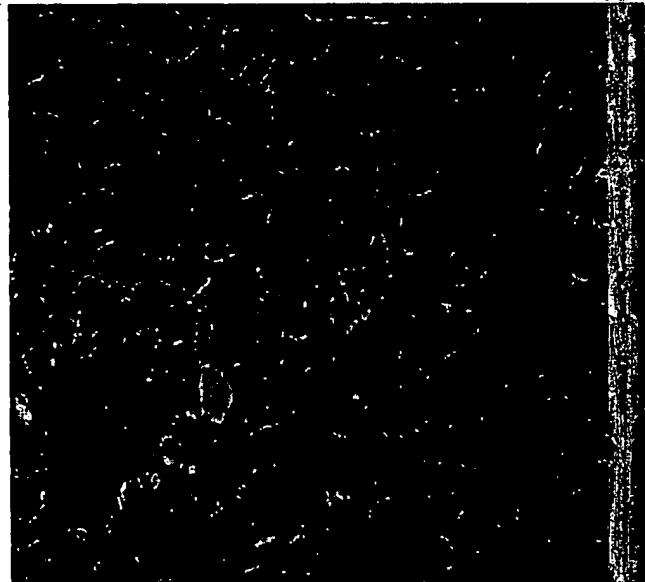


FIG. 2D



FIG. 2E

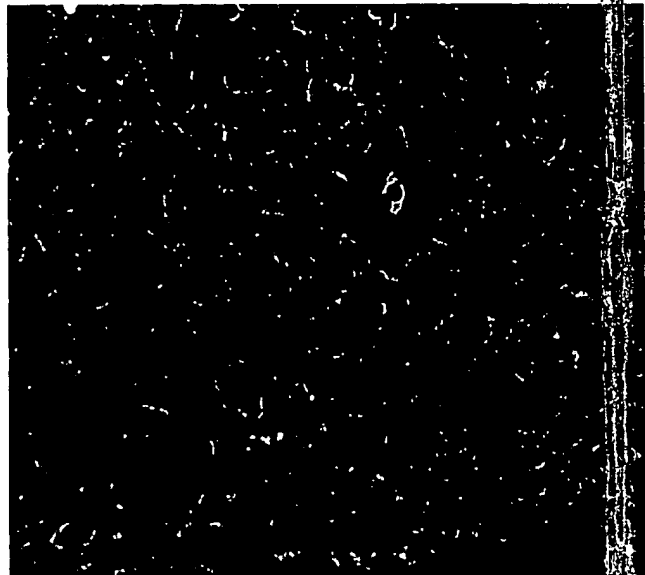


FIG. 2F

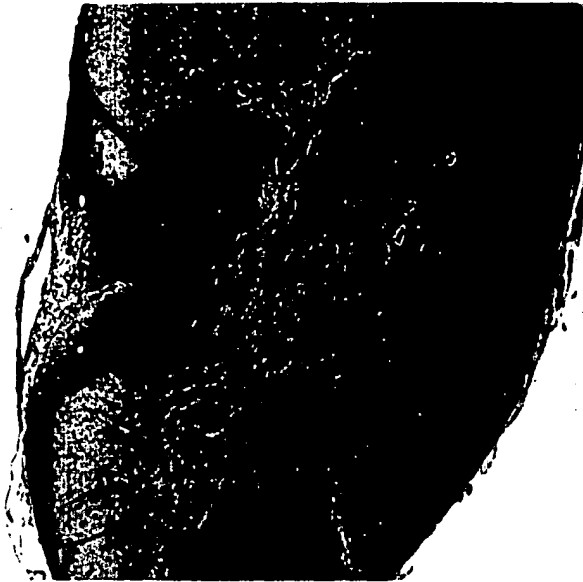


FIG. 2G

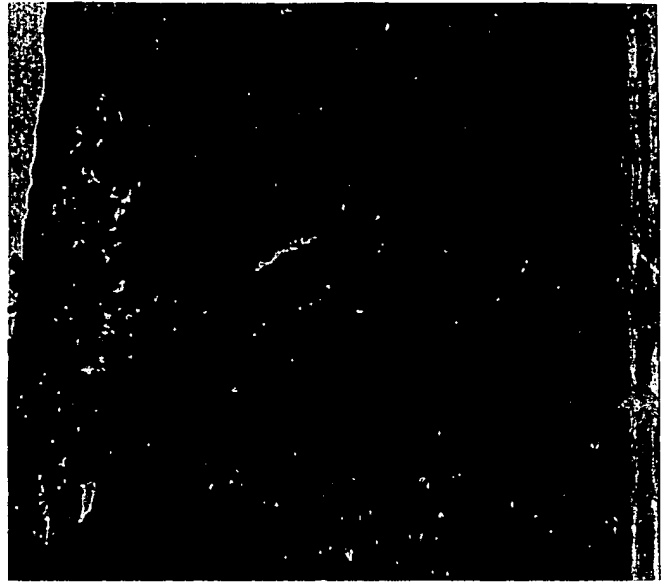


FIG. 2H



FIG. 2I



FIG. 2J

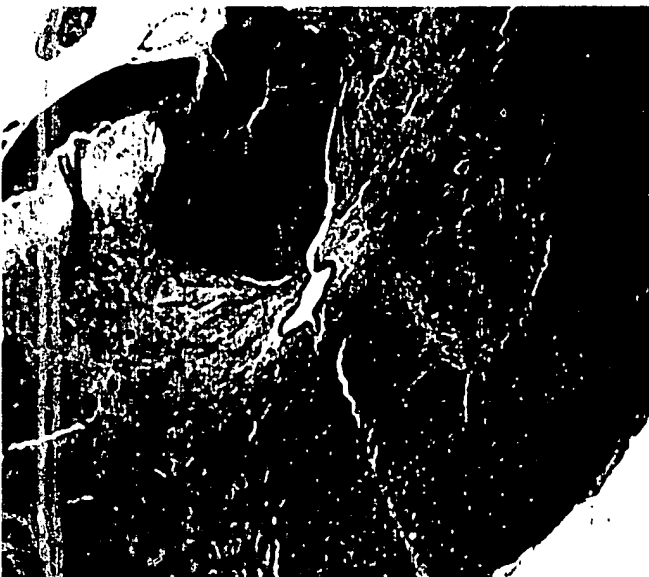
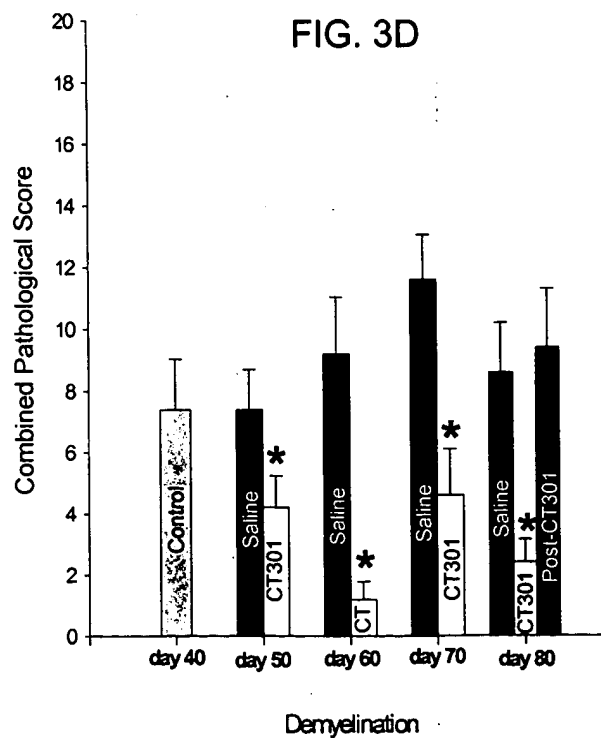
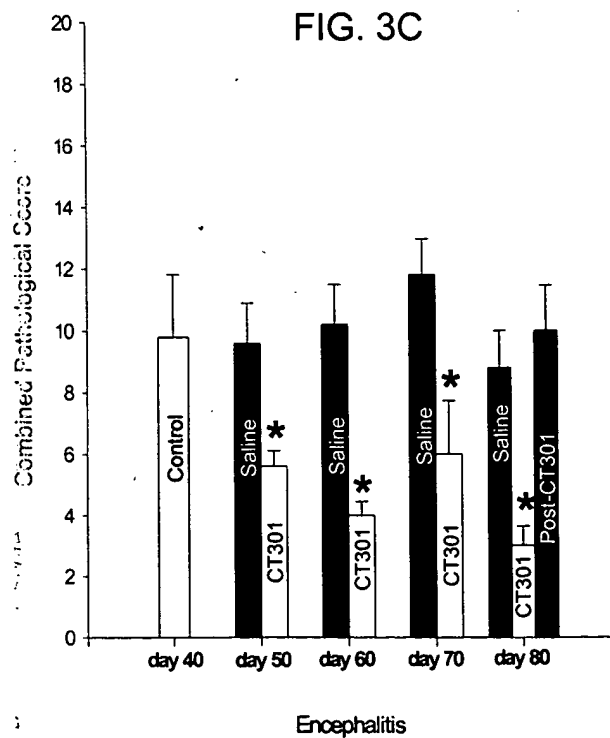
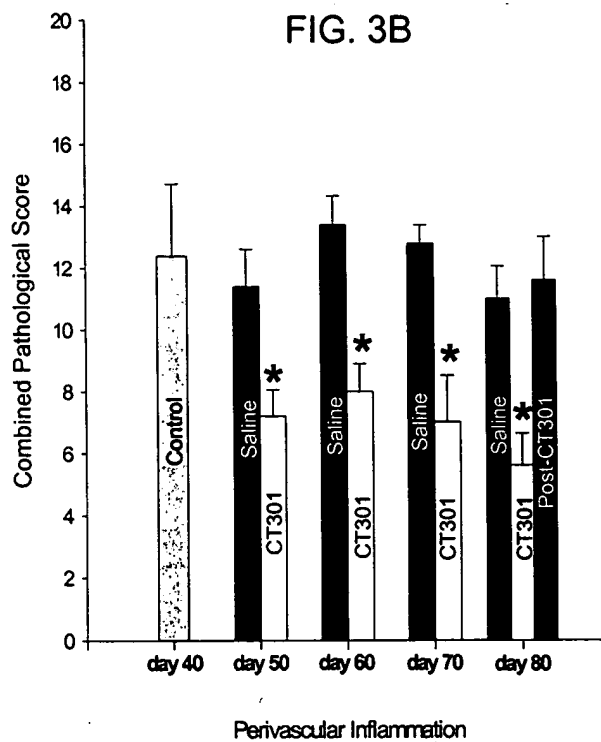
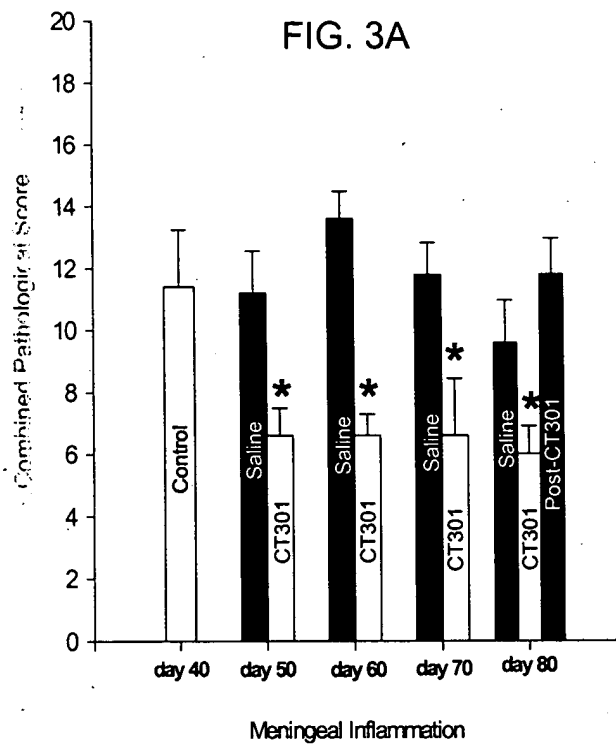


FIG. 2K



FIG. 2L



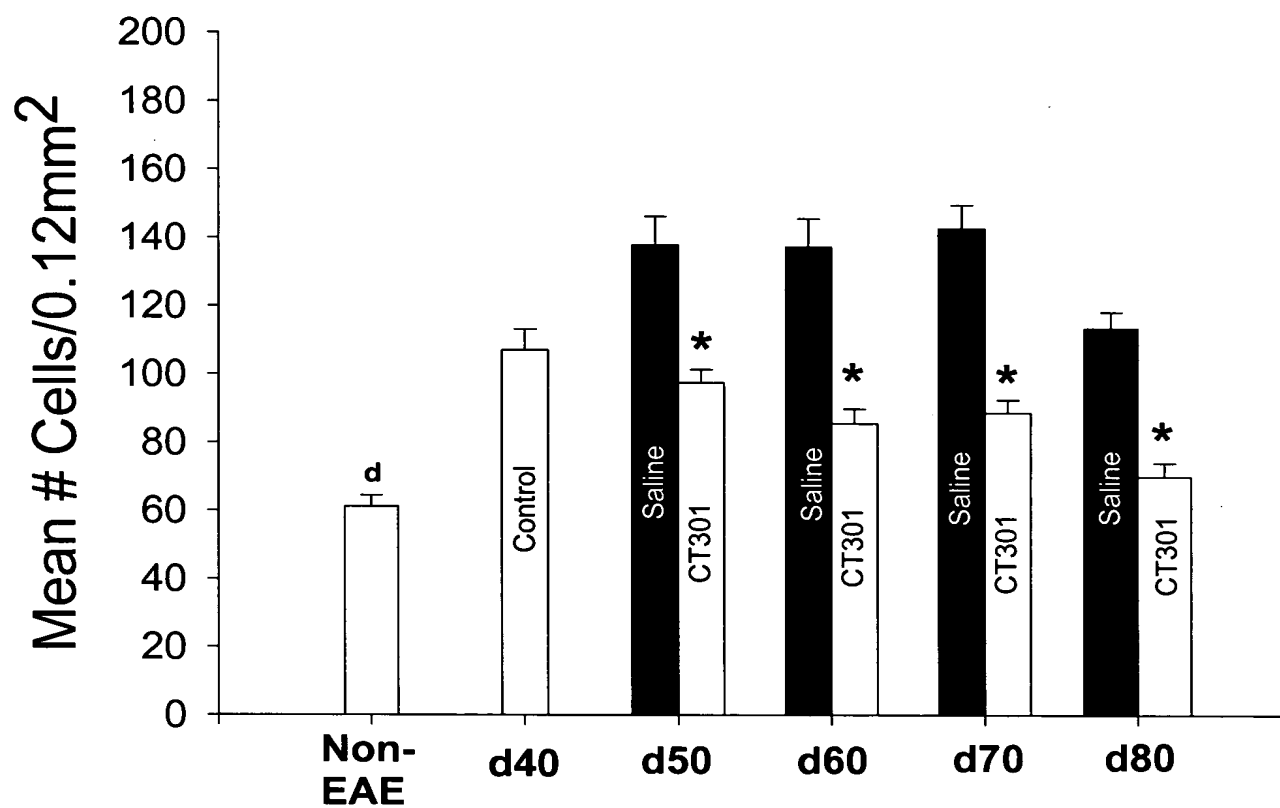
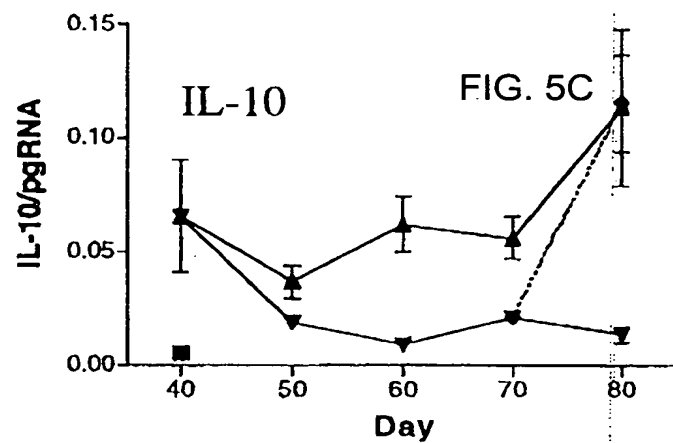
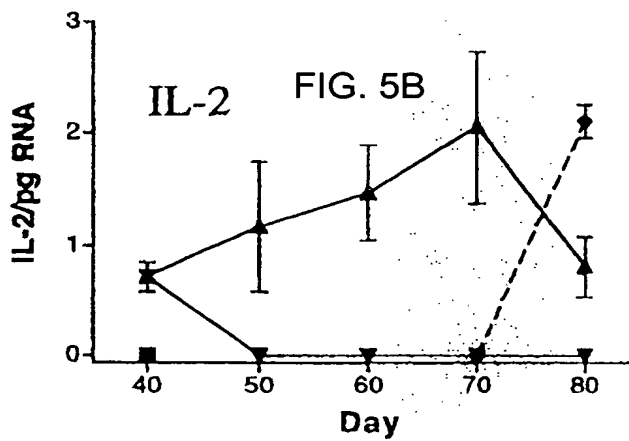
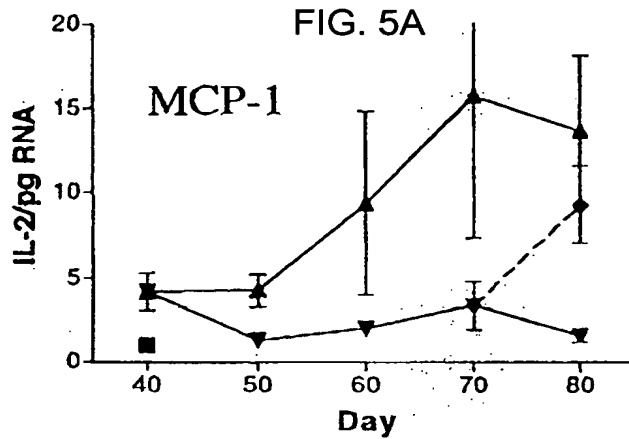
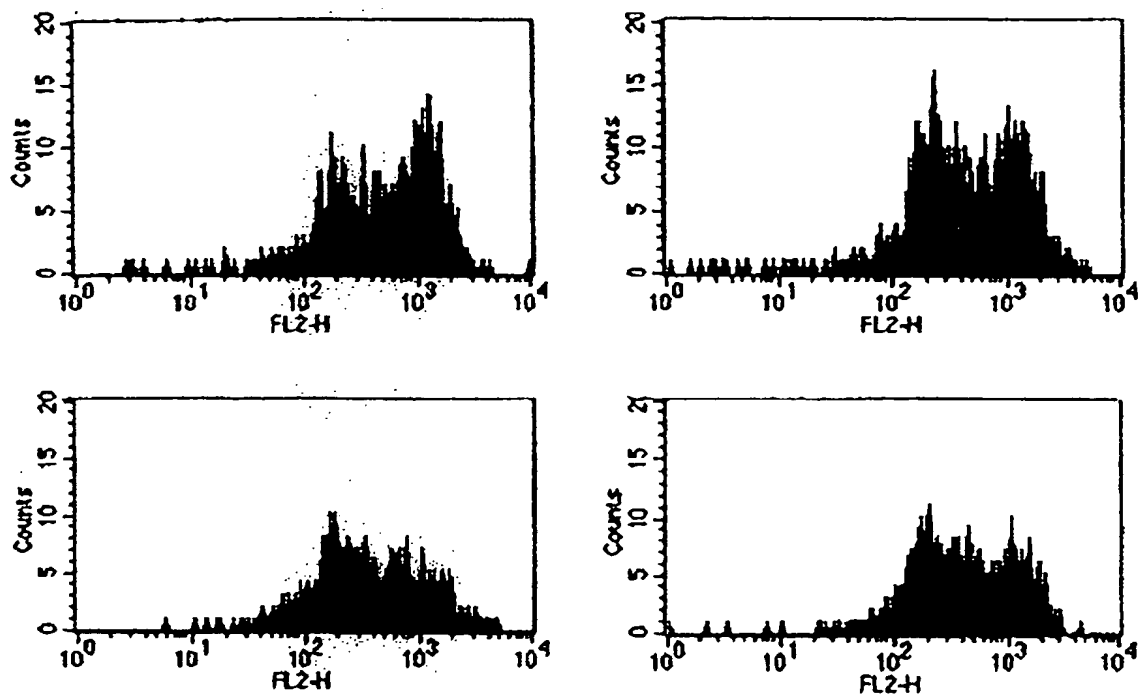


FIG. 4



CT301



Saline

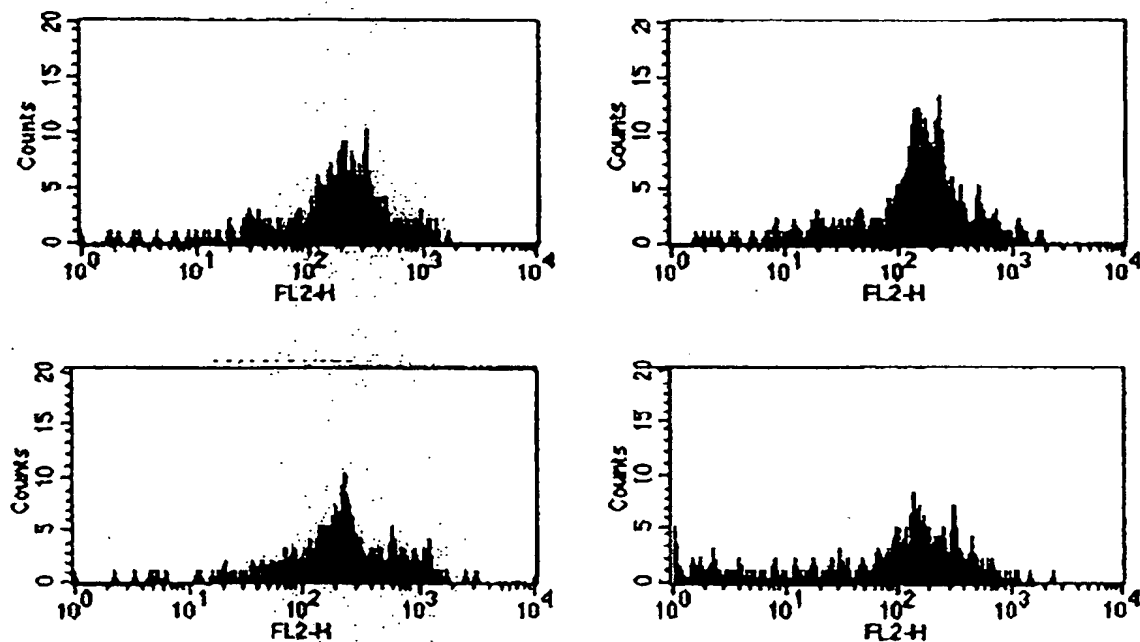


FIG. 6

Percentage $\alpha 4$ Integrin-High Blood Lymphocytes

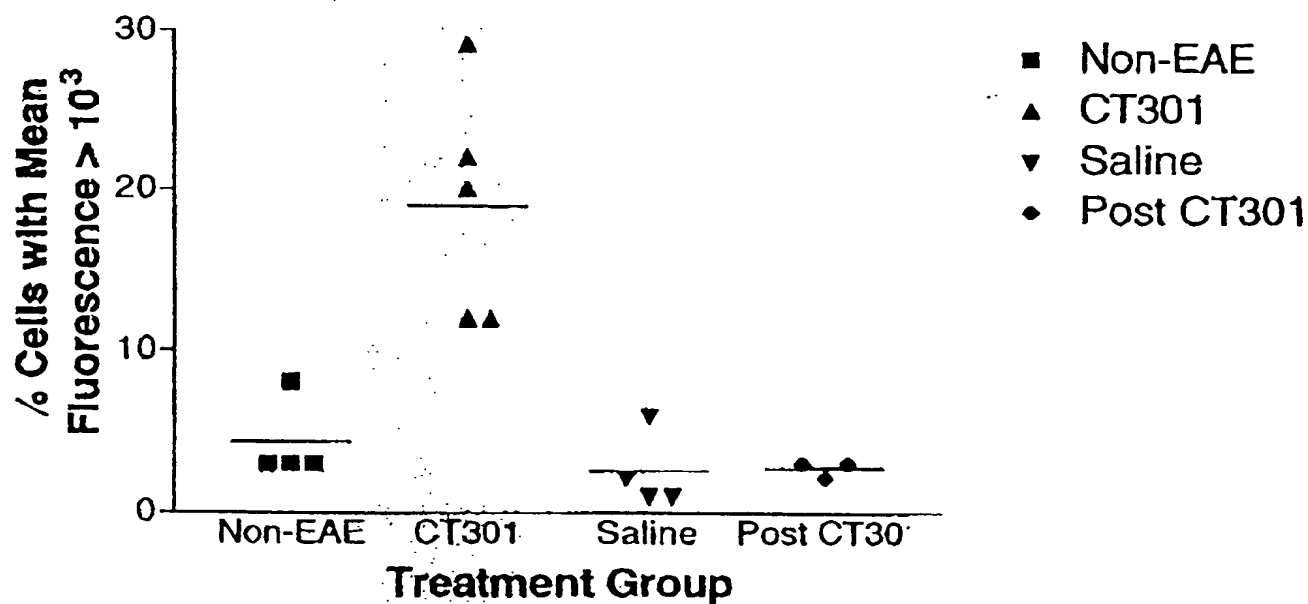


FIG. 7A

Expression of $\alpha 4$ Integrin on Blood Monocytes

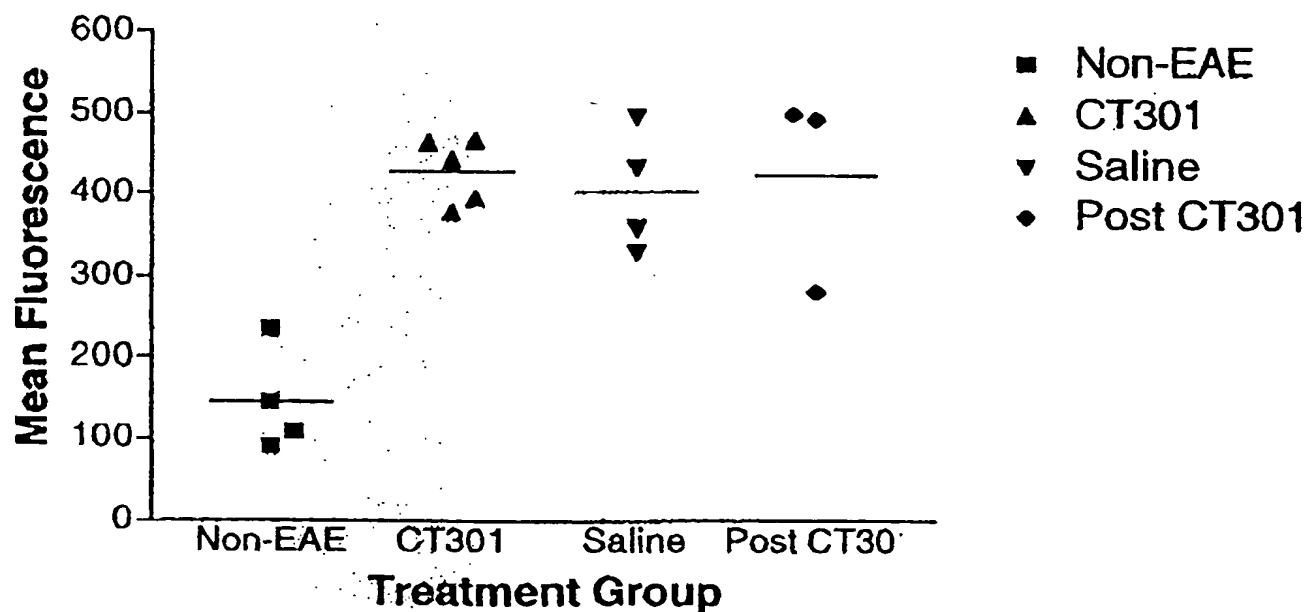


FIG. 7B

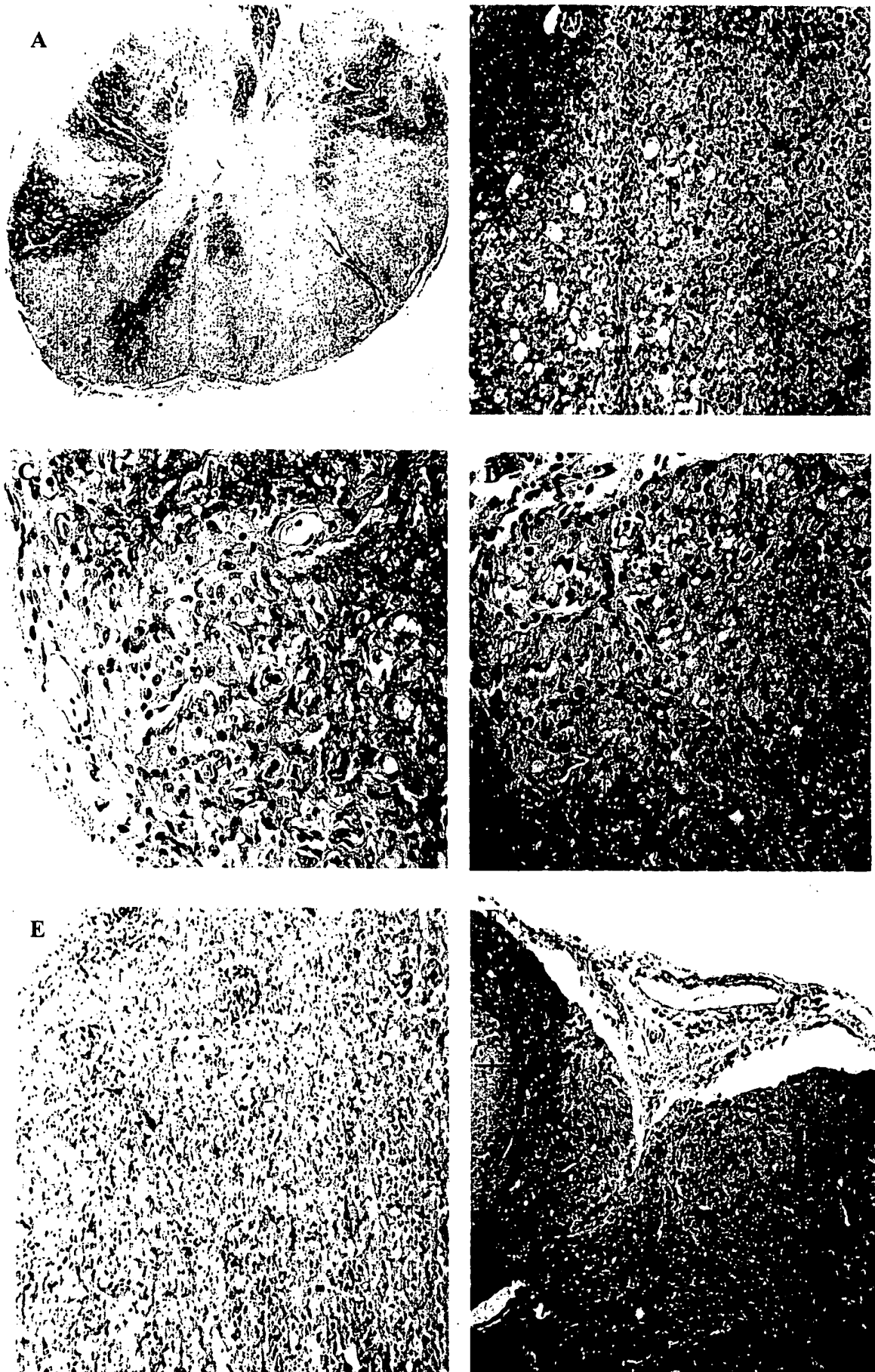


FIG. 8

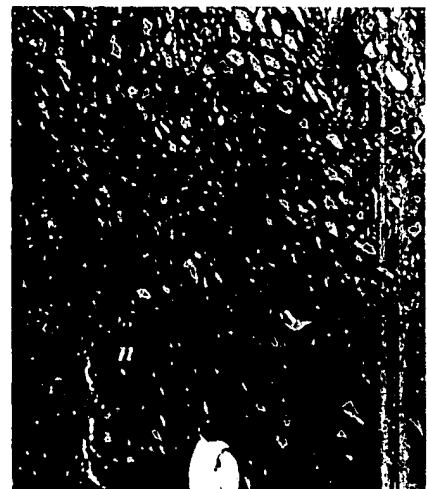
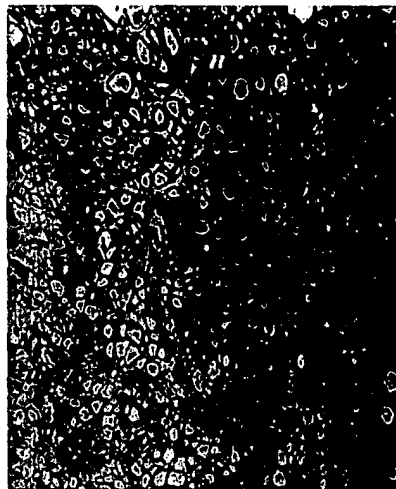
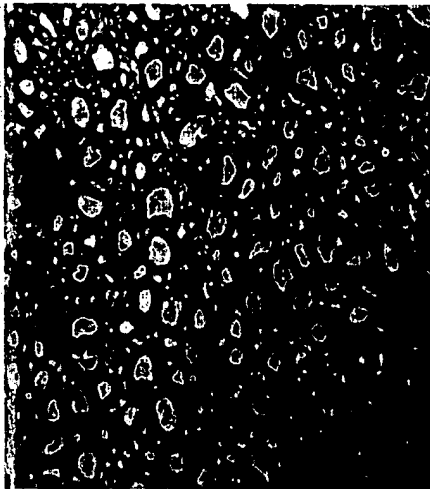


FIG. 9

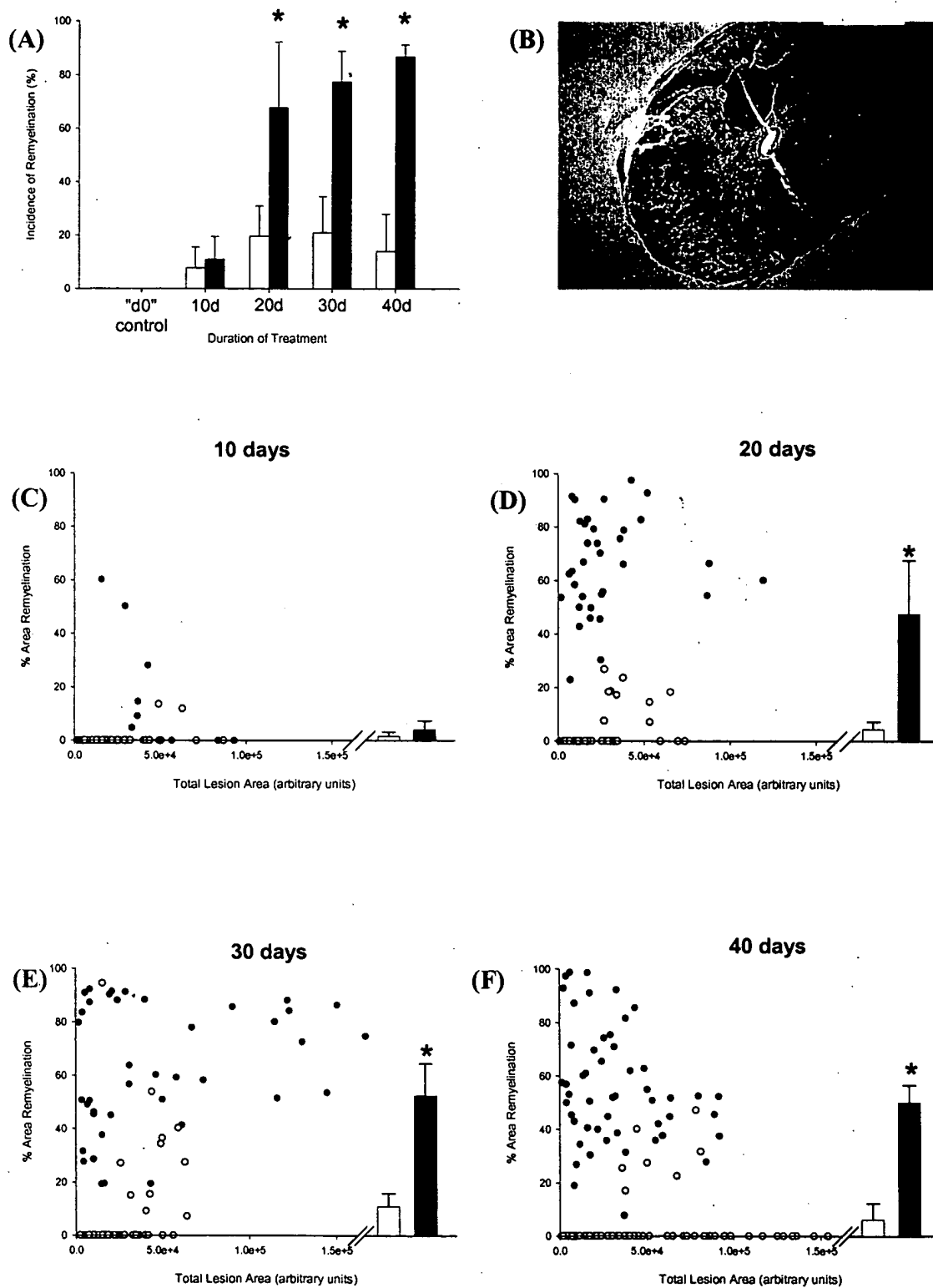


FIG. 10

1 atgagggccctgctcagatTTTTGGATTCTTGGTCAGGAGACGTTGT

tactcccggggacgagtctaaaaacctaagaaccagtcctctgcaaca

49 agaaatgagaccgtctattcagttcctggggctcttggtgttctggcttcattgg

tctttactctggcagataagtcaggaccccgagaacaacaagaccgaagtacc

(M R P S I Q F L G L L L F W L H G
LEADER

103 tgctcagtggtgacatccagatgacacagttctccatcctcactgtctgcatctct

acgagtcacactgtaggcttactgtgtcagaggtaggagtgcagagcgtagaga

A Q C)[D I Q M T Q S P S S L S A S L
FR1

157 gggaggcaaagtcccatcacttgcaagacaagccaagacattaacaagtatat

ccctccgtttcagtggttagtgaacggttctgttcggttctgtaattgttcataata

G G K V T I T C)[K T S Q D I N K Y M
CDR1

211 ggcttggtaccaacacaagcctggaaaacgtcctagggtggtcatacattacac

ccgaaccatggttggttcggaccttttgcaggatccgacgagtatgtaattgtg

A)[W Y Q H K P G K R P R L L I H][Y T
FR2

265 atctgcattacagccaggcatcccatcaagggttcagtggaagtgggtctgggag

tagacgtaattgtcgggtccgtagggttagttccaagtcaccttcacccagaccctc

S A L Q P)[G I P S R F S G S G S G R
CDR2

FIG. 11 A

319 agattattccttcaacatcagcaacctggagcctgaagatattgcaacttatta

tctaataaggaagttgtagtcgctggacctcggacttctataaacgctgaataat

D Y S F N I S N L E P E D I A T Y Y
FR3

373 ttgtctacagtatgataatctgtggacgcttcggtggaggcaccaagctggaaat

aacagatgtcatactattagacacctgcaagccacctccgtggttcgaccttta

C)[L Q Y D N L W T][F G G G T K L E I
CDR3 FR4

427 caaacgggctgatgctgcaccaactgtatccatcttcccaccatccacccggga

gtttgcccgactacgacgtggttgacataggtagaagggtggtagggtgggcctt

K]

AGG-5'
tcc
481 ---
agg

FIG. 11B

1 atgaaatgcagctgggtcatgttcttcctgatggcagtggttacaggg

tactttacgtcgacccagttacaagaaggactaccgtcaccaatgtccc

[M K C S W V M F F L M A V V T G
LEADER

49 gtcaattcagaggttcagctgcagcagtcctggggcagagcttgtgaagccaggg

cagttaagtctccaagtcgacgtcgtcagaccccgctcgaacacttcgggtccc
V N S][E V Q L Q Q S G A E L V K P G
FR1

103 gcctcagtcagttgtcctgcacagcttctggcttcaacattaaagacacctat

cggagtcagttcaacaggacgtgtcgaagaccgaagttgtaatttctgtggata
A S V K L S C T A S G F N I K][D T Y
CDR1

157 atacactgtgtgaagcagaggcctgaacagggcctggagtggttggaaggatt

tatgtgacacacttcgtctccggacttgtcccggacctcacctaaccttcctaa
I H][C V K Q R P E Q G L E W I G][R I
FR2

211 gatcctgcgaatggttataactaaatatgacccgaagttccagggcaaggccact

ctaggacgcttaccaatatgatttatactgggcttcaagggtcccgttccgggtga
D P A N G Y T K Y D P K F Q G][K A T
CDR2

265 ataacagctgacacatcctccaacacagcctacctgcagctcagcagcctgaca

tattgtcgactgtgtaggaggttgtgtcggtatggacgtcgagtcgtcggactgt
I T A D T S S N T A Y L Q L S S L T
FR3

FIG. 12A

319 tctgaggacactgccgtctatttctgtgctagagaggatattatggtaactac

agactcctgtgacggcagataaagacacgatctctccctataataaccattgatg
S E D T A V Y F C A R][E G Y Y G N Y
CDR3.

373 ggggtctatgctatggactactgggggtcaaggaacctcagtcaccgtctcctca

ccccagatacagatacctgatgaccccagttccttggagtcagtggcagaggagt
G V Y A M D Y][W G Q C T S V T V S S]

427 gccaaaacgacacccccatctgtctatccactggcccgggatcc

cggtttttgctgtgggggtagacagataggtgaccgggcctagg
S S]

FIG. 12B

	FR1		CDR1		FR2		CDR2
	1	2	3		4	5	
	12345678901234567890123	45678901234	5678901234		567890123456789	0123456	
	*		*****		*	***	
21.6	DIQMTQSPSSLSASLGGKVTITC	KTSQDINKYMA	WYQHKPGKRPRLLIH	YTSALQP			
REI	DIQMTQSPSSLSASVGDRTITC	QASQDIKYLN	WYQQTGKAPKLLIY	EASNLQA			
La	DIQMTQSPSSLSASVGDRTITC	KTSQDINKYMA	WYQQTGKAPRLLIH	YTSALQP			
Lb	-----R-----						

	FR3		CDR3		FR4
	6	7	8	9	10
	78901234567890123456789012345678	901234567	8901234567		
	*	*	*****		
21.6	GIPSRFSGSGSGRDYSFNISNLEPEDIATYYC	LQYDNL-WT	FGGGTKLEIK		
REI	GVPSRFSGSGSGTDYFTISSLQPEDATYYC	QQYQSLPYT	FGQGTLQIT		
La	GIPSRFSGSGSGRDYFTISSLQPEDATYYC	LQYDNL-WT	FGQGTVKVEIK		
Lb	-I-----R-----VE-K				

FIG. 13

	FR1										CDR1					FR2					CDR2				
	1		2		3		4		5		6														
	123456789012345678901234567890	12345	6789012345	6789012345	6789012345	6789012345	6789012345	6789012345	6789012345	6789012345	6789012345	6789012345	6789012345	6789012345	6789012345	6789012345	6789012345	6789012345	6789012345	6789012345					
	*****										***					****									
21.6	EVQLQQSGAELVKPGASVKLSCTASGFNIK										DTYIH					CVKQRPEQGLEWIG					RIDPANGYTKYDPKFQG				
2*CL	QVQLVQSGAEVKKPGASVKVSCKASGYTFT										SYAMH					WVRQAPGQRLEWMG					WINAGNGNTKYSQKFQG				
Ha	QVQLVQSGAEVKKPGASVKVSCKASGFNIK										DTYIH					WVRQAPGQRLEWMB					RIDPANGYTKYDPKFQG				
Hb	-----FNIK										-----G-----														
Hc	-----FNIK										-----					-----									

	FR3										CDR3					FR4									
	7		8		9		10		11																
	67890123456789012345678901234	56789012345678901234	56789012345678901234	56789012345678901234	56789012345678901234	56789012345678901234	56789012345678901234	56789012345678901234	56789012345678901234	56789012345678901234	56789012345678901234	56789012345678901234	56789012345678901234	56789012345678901234	56789012345678901234	56789012345678901234	56789012345678901234	56789012345678901234							
	*										*														
21.6	KATITADTSSNTAYLQLSSLTSED										TAVYFCAR					EGYYGNYGVYAMDY					WGQGTSTVTVSS				
2*CL	RVTITRDTASTAYMELSSLRSED										TAVYYCAR					GGYYGSGS----					NY WGQGTSLVTVSS				
Ha	RVTITADTASTAYMELSSLRSED										TAVYYCAR					EGYYGNYGVYAMDY					WGQGTSLVTVSS				
Hb	-----A-----										-----					-----									
Hc	-----A-----										-----F-----					-----									

FIG. 14

HindIII KOZAK SEQUENCE
1 aagccttgcgccaccargagaccgtctattcagttcctggggctcttggtgttc

ttcgaacggcggtggtactctggcagataagtcaaggaccccgagaacaacaag
[M R P S I Q F L G L L L F
LEADER
55 tggcttcattggtgctcagtggtgacatccagatgacacagttccatcctcactg

accgaagtaccacgagtcacactgtaggtctactgtgtcagaggtaggagtgc
W L H G A Q C][D I Q M T Q S P S S L
FR1
109 tctgcatctGTAggaGATAGAgtcaccatcacttgcaagacaagccaagacatt

agacgtagaCATcctCTATCTcagtggtagtgaacggttctgttcggttctgtaa
S A S V G D R V T I T C][K T S Q D I
CDR1
163 aacaagtatatggccttggtaccaaCAGACAcctggaaaaGCTcctaggctgctc

ttgttcataataccgaaccatgggtGTCTGTggaccttttCGAggatccgacgag
N K Y M A)[W Y Q Q T P G K A P R L L
FR2
217 atacattacacatctgcattacagccaggcatcccatcaagggttcagtggaagt

tatgtaatgtgtagacgtaatgtcggtccgtagggtagttccaagtcaccttca
I H)[Y T S A L Q P][G I P S R F S G S
CDR2
271 gggctctgggagagattatACTttcACCatcagcAGCctgCAGcctgaagatatt

cccagaccctctctaataTGAaagTGGtagtcgTCGgacGTCggacttctataa
G S F R D Y T F T I S S L Q P E D I
FR3

FIG. 15A

325 gcaacttattattgtctacagtatgataatctgtggacgttcggtCAAggcacc

cgttgaataataacagatgtcatactattagacacctgcaagccaGTTccgtgg

A T Y Y C)[L Q Y D N L W T][F G Q G T
CDR3 FR4

SPLICE DONOR SITE BamHI
aagGTGgaaatcaaacgtgagtgatcc
379 -----
ttcCACcttttagtttgactcacctagg

K V E I K]

FIG. 15B

HindIII KOZAK SEQUENCE
AAGCTTGCCGCCACCATGGACTGGACCTGGCGCGTGTTTTGCCTGCTCGCCGTG
1 -----
TTCGAACGGCGGTGGTACCTGACCTGGACCGCGCACAAACGGACGAGCGGCAC
[M D W T W R V F C L L A V
LEADER
GCTCCTGGGGCCACAGCCAGGTGCAACTAGTGCAGTCCGGCGCCGAAGTGAAG
55 -----
CGAGGACCCCGGGTGTCTGGTCCACGTTGATCACGTCAGGCCGCGGCTTCACTTC
A P G A H S][Q V Q L V Q S G A E V K
AAACCCGGTGCTTCCGTGAAAGTCAGCTGTAAAGCTAGCGGTttcaacattaaa
109 -----
TTTGGGCCACGAAGGCACTTTTCAGTCGACATTTTCGATCGCCAaagttgtaattt
K P G A S V K V S C K A S G F N I K][
FR1
gacacctatatacactGGGTTAGACAGGCCCCctGGCCAAaGGCTgGAGTGGATg
163 -----
ctgtggatatatgtgACCCAATCTGTCCGGgGaCCGGTTtCCGAcCTCACCTAc
D T Y I H][W V R Q A P G Q R L E W M
CDR1 FR2

FIG. 16A

217 GGAaggattgatcctgcgaatggttataactaaatatgacccgaagttccagggc

CCTtcctaactaggacgcttaccaatatgattttatactgggcttcaaggtcccg
G)[R I D P A N G Y T K Y D P K F Q G)]
CDR2

271 cgggtcACCAcAcACCGcaGACACCTCTgccagcACCGCCTACATGGAACGTGCC

gcccagTGGtagTGGcgtCTGTGGAGAcggtcgTGGCGGATGTACCTTGACAGG
R V T I T A D T S A S T A Y M E L S
FR3

325 AGCCTGCGCTCCGAGGACACTGCAGTCTACTACTGCGCCagagagggatattat

TCGGACGCGAGGCTCCTGTGACGTCAGATGATGACGCGGtctctccctataata
S L R S E D T A V Y Y C A R)](E G Y Y
ggtaactacggggtctatgctatgGACTAcTGGGGtCAaGGaACCCTTGTCACC
379 -----
ccattgatgccccagatacagatacCTGATgACCCCaGtCCtTGGGAACAGTGG
G N Y G V Y A M D Y)](W G Q G T L V T
CDR3 FR4

SPLICE DONOR SITE BamHI
433 GTCTcctCAGGTGAGTGGATCC

CAGaggAGTCCACTCACCTAGG
V S S]

FIG. 16B

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

N - Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Asp Ile Ser Asn
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ser Pro Lys Leu Leu
Ile Tyr Tyr Ala Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser
Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu
Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro
Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys - C

FIG. 17A

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

N - Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ser Leu Val Xaa
Xaa Ser Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
Tyr Asn Ser Leu Pro Glu Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
Ile Lys - C

FIG. 17B

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein

N - Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
Gly Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Tyr Asp Pro Lys Phe
Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
Ala Arg Gly Tyr Tyr Tyr Tyr Asp Ser Xaa Val Gly Tyr Tyr Ala Met
Asp Tyr Trp Gly Gln Gly Thr Xaa Val Thr Val Ser Ser - C

FIG. 18A

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

N - Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
Gly Trp Ile Asn Pro Tyr Gly Asn Gly Asp Thr Asn Tyr Ala Gln Lys
Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser Thr Ala
Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr
Cys Ala Arg Ala Pro Gly Tyr Gly Ser Gly Gly Gly Cys Tyr Arg Gly Asp
Tyr Xaa Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser - C

FIG. 18B